PATENT
Attorney Docket No.: A-70586-1/RFT/RMS/RMK

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

SPRINGER et al.

Serial No. 09/902,481

Filed: July 9, 2001

For: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY

Examiner: UNKNOWN

Group Art Unit: 1653

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service as First Class Mail in an envelope addressed to: Assistant Commissioner of Patents, BOX SEQUENCE, Washington, DC 20231 on 3-4-02, ~~2001~~.

Signed: Marjorie Jost
Marjorie Jost

PRELIMINARY AMENDMENT RE SEQUENCE LISTING

Assistant Commissioner for Patents
BOX SEQUENCE
Washington, DC 20231

Sir:

This Amendment is in anticipation of a Notice to Comply with Requirements for Patent Applications Containing Nuclectide Sequence And/or Amino Acid Sequence Disclosures and in compliance with 37 C.F.R. § 1.821-1.825. Although no fee is believed to be due at this time, the Commissioner is authorized to charge any fees including extension fees or other relief which may be required, or credit any overpayment to Deposit Account No. 06-1300 (Our Order No. A-70586-1-1/RFT/RMS/RMK).

Please amend the application as follows to comply with requirements for patent applications containing nucleotide sequence and/or amino acid sequence disclosures in adherence with rules 37 C.F.R. § 1.821-1.825:

IN THE SPECIFICATION:

Please replace the paragraph beginning at page 5, line 30, with the following rewritten paragraph:

– Figure 1. Stereoview of mutations in the Mac-1 I-domain open structures (active/high affinity/ido). Fig 1A depicts wild type 1ido (open) structure. Fig. 1B depicts the structure computed for the ido1q (open) mutant. Fig 1C depicts the structure computed for the ido1r (open) mutant. Fig 1D depicts the structure computed for the ido2r (open) mutant. Mutant sequences and rotamers were computed as described herein. A cavity was detected in the wild-type 1ido structure but not in the designed mutants, using VOIDOO (Kleywegt et al., Acta Cryst D50:178-185 (1994)) (with a probe of 1.4 Å, a van der Waals growth factor of 1.1, and a minimum of 5 voxels. The cavity is 202 $Å^3$ in 1ido. The cavity is filled by mutations V238F and V160I in ido1q (Fig 1B), V238F and F156W in ido1r (Fig 1C), and V238I in ido2r (Fig 1D). Figure made with Ribbons (Carson, Methods in Enzymology 277:493-505). Fig 1E is a cartoon representation of a complete integrin heterodimer. The black circles represent bivalent cation binding sites. Fig 1F depicts the amino acid sequence of Mac-1 alpha subunit of integrin (SEQ ID NO:1). Fig 1G depicts the nucleotide sequence of Mac-1 alpha subunit of integrin (SEQ ID NO:2). –

Please replace paragraph beginning at page 21, line 28, with the following rewritten paragraph:

– The variant integrin proteins and nucleic acids of the invention are distinguishable from naturally occurring integrins. By "naturally occurring" or "wild type" or grammatical equivalents, herein is meant an amino acid sequence or a nucleotide sequence that is found in nature and includes